

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/S39,443
Source: TFWP
Date Processed by STIC: 08/07/2006

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 08/07/2006
PATENT APPLICATION: US/10/539,443 TIME: 09:43:36

Input Set : A:\SequenceListing.ST25.txt
Output Set: N:\CRF4\08072006\J539443.raw

3 <110> APPLICANT: Aarhus University
5 <120> TITLE OF INVENTION: Modulation of activity of neurotrophins
7 <130> FILE REFERENCE: P700PC00
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,443
C--> 9 <141> CURRENT FILING DATE: 2005-06-20
9 <160> NUMBER OF SEQ ID NOS: 13
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 831
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
20 Met Glu Arg Pro Trp Gly Ala Ala Asp Gly Leu Ser Arg Trp Pro His
21 1 5 10 15
24 Gly Leu Gly Leu Leu Leu Leu Gln Leu Leu Pro Pro Ser Thr Leu
25 20 25 30
28 Ser Gln Asp Arg Leu Asp Ala Pro Pro Pro Ala Ala Pro Leu Pro
29 35 40 45
32 Arg Trp Ser Gly Pro Ile Gly Val Ser Trp Gly Leu Arg Ala Ala Ala
33 50 55 60
36 Ala Gly Gly Ala Phe Pro Arg Gly Gly Arg Trp Arg Arg Ser Ala Pro
37 65 70 75 80
40 Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val Ala Lys Leu
41 85 90 95
44 Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg Gly Ser Val
45 100 105 110
48 Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu Val Leu Thr
49 115 120 125
52 Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln Ser Lys Leu
53 130 135 140
56 Tyr Arg Ser Glu Asp Tyr Gly Lys Asn Phe Lys Asp Ile Thr Asp Leu
57 145 150 155 160
60 Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala Ile Gly Pro
61 165 170 175
64 Glu Asn Ser Gly Lys Val Val Leu Thr Ala Glu Val Ser Gly Gly Ser
65 180 185 190
68 Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys Asn Phe Val
69 195 200 205
72 Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met Tyr Ser Pro
73 210 215 220
76 Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn Gly Leu Trp
77 225 230 235 240
80 Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His Lys Ala Val

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81	245	250	255
84	Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe Thr Thr Tyr		
85	260	265	270
88	Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly Ala Leu Glu Leu Trp Arg		
89	275	280	285
92	Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val Lys Ile Tyr		
93	290	295	300
96	Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val Met Ala Asp		
97	305	310	315
100	315	320	
101	Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln Gly Asp Thr		
104	325	330	335
105	Trp Ser Met Ala Gln Leu Pro Ser Val Gly Gln Glu Gln Phe Tyr Ser		
108	340	345	350
109	Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp Glu Pro		
112	355	360	365
113	Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg Gly Ile		
116	370	375	380
117	Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Gly Gly		
119	385	390	395
120	400		
121	Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr Ile Thr		
124	405	410	415
125	Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile Thr Phe Asp		
128	420	425	430
129	Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser Glu Cys		
132	435	440	445
133	Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile His Ala		
136	450	455	460
137	Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala Pro Leu Ser		
140	465	470	475
141	Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val Gly Asp		
144	485	490	495
145	Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp Asp Gly Gly		
148	500	505	510
149	Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr Ile Leu		
152	515	520	525
153	Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser Arg Pro Ile		
156	530	535	540
157	Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp Gln Thr Tyr		
160	545	550	555
161	Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala Ser Glu Pro		
164	565	570	575
165	Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr Glu Ser Phe		
168	580	585	590
169	Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys Asp Ile Leu		
172	595	600	605
173	Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu Ala His Ser		
176	610	615	620
177	Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly Tyr Lys Glu		
	625	630	635
			640

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180 Gln Phe Leu Arg Leu Arg Lys Ser Ser Met Cys Gln Asn Gly Arg Asp
181 645 650 655
184 Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser Leu Glu Asp
185 660 665 670
188 Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp Ser Lys Cys
189 675 680 685
192 Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe Cys Leu Tyr
193 690 695 700
196 Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys Ile Pro Gly
197 705 710 715 720
200 Asp Lys Cys Gln Gly Val Asn Pro Val Arg Glu Val Lys Asp Leu
201 725 730 735
204 Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys Gln Asn Ser
205 740 745 750
208 Lys Ser Asn Ser Val Pro Ile Ile Leu Ala Ile Val Gly Leu Met Leu
209 755 760 765
212 Val Thr Val Val Ala Gly Val Leu Ile Val Lys Lys Tyr Val Cys Gly
213 770 775 780
216 Gly Arg Phe Leu Val His Arg Tyr Ser Val Leu Gln Gln His Ala Glu
217 785 790 795 800
220 Ala Asn Gly Val Asp Gly Val Asp Ala Leu Asp Thr Ala Ser His Thr
221 805 810 815
224 Asn Lys Ser Gly Tyr His Asp Asp Ser Asp Glu Asp Leu Leu Glu
225 820 825 830
228 <210> SEQ ID NO: 2
229 <211> LENGTH: 2214
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 2
235 Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
236 1 5 10 15
239 Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
240 20 25 30
243 Gln Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe
244 35 40 45
247 Leu Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly
248 50 55 60
251 Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys
252 65 70 75 80
255 Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
256 85 90 95
259 Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
260 100 105 110
263 Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
264 115 120 125
267 Arg Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
268 130 135 140
271 Phe Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser
272 145 150 155 160

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275 Glu Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
276 165 170 175
279 Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
280 180 185 190
283 Phe Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
284 195 200 205
287 Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
288 210 215 220
291 Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
292 225 230 235 240
295 Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp
296 245 250 255
299 Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser
300 260 265 270
303 Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu
304 275 280 285
307 Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp
308 290 295 300
311 Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Leu Gly Ser Glu Gln
312 305 310 315 320
315 Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg
316 325 330 335
319 Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala
320 340 345 350
323 Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn
324 355 360 365
327 Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu
328 370 375 380
331 Ser Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp
332 385 390 395 400
335 Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg
336 405 410 415
339 Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser
340 420 425 430
343 Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly
344 435 440 445
347 Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys
348 450 455 460
351 Ile Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg
352 465 470 475 480
355 Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser
356 485 490 495
359 Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys
360 500 505 510
363 Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala
364 515 520 525
367 Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp
368 530 535 540
371 His Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu

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372	545	550	555	560
375	Leu Lys Tyr Ser Thr Asn Glu Gly Glu	Thr Trp Lys Thr Phe Ile Phe		
376	565	570	575	
379	Ser Glu Lys Pro Val Phe Val Tyr Gly Leu	Leu Thr Glu Pro Gly Glu		
380	580	585	590	
383	Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys	Glu Asn Val His		
384	595	600	605	
387	Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala	Leu Gly Val Pro		
388	610	615	620	
391	Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly			
392	625	630	635	640
395	Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg	Thr Pro		
396	645	650	655	
399	His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val			
400	660	665	670	
403	Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe			
404	675	680	685	
407	Lys Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu			
408	690	695	700	
411	Phe Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser			
412	705	710	715	720
415	Thr Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys			
416	725	730	735	
419	Ser Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys			
420	740	745	750	
423	Pro Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser			
424	755	760	765	
427	Ile Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu			
428	770	775	780	
431	Thr Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn			
432	785	790	795	800
435	Cys Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys			
436	805	810	815	
439	Leu Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu			
440	820	825	830	
443	Thr Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp			
444	835	840	845	
447	Val Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp			
448	850	855	860	
451	Phe Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala			
452	865	870	875	880
455	Leu Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly			
456	885	890	895	
459	Asp Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala			
460	900	905	910	
463	Tyr His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val			
464	915	920	925	
467	Asp Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu			
468	930	935	940	

VERIFICATION SUMMARY

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Input Set : A:\SequenceListing.ST25.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date